

Appl. No.: 10/796,307
Atty. Docket: CI.1509ORD

AMENDMENTS TO THE CLAIMS

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This listing of claims will replace all prior versions, and listings of claims in the application.

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Listing of claims

1. (Currently amended) A method for identifying an individual a human who has an altered risk for developing myocardial infarction, comprising detecting a single nucleotide polymorphism (SNP) as represented by a the nucleotide sequence selected from the group consisting of SEQ ID NOS 33944, 21614, 36349, 25917, 21749, 29108, 27819, 10810, 11670, 28735 in said individual's human nucleic acids, wherein the presence of the SNP is correlated with an altered risk for myocardial infarction in said individual human.
2. (Original) The method of claim 1 in which the altered risk is an increased risk.
3. (Original) The method of claim 2 in which said individual has previously had a myocardial infarction.
4. (Original) The method of claim 1 in which the altered risk is a decreased risk.
5. (Canceled)
6. (Original) The method of claim 1 in which detection is carried out by a process selected from the group consisting of: allele-specific probe hybridization, allele-specific primer extension, allele-specific amplification, sequencing, 5' nuclease digestion, molecular beacon assay, oligonucleotide ligation assay, size analysis, and single-stranded conformation polymorphism.
- 7.-20. (Canceled)
21. (Currently amended) A method of detecting a single nucleotide polymorphism (SNP) in a nucleic acid molecule, comprising contacting a test sample with a reagent which specifically

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hybridizes to a the SNP as represented by a the nucleotide sequence selected from the group consisting of SEQ ID NOS 33944, 21614, 36349, 25917, 21749, 29108, 27819, 10810, 11670, 28735 under stringent hybridization conditions, and detecting the formation of a hybridized duplex, thereby indicating the presence of said SNP.

22. (Original) The method of claim 21 in which detection is carried out by a process selected from the group consisting of: allele-specific probe hybridization, allele-specific primer extension, allele-specific amplification, sequencing, 5' nuclease digestion, molecular beacon assay, oligonucleotide ligation assay, size analysis, and single-stranded conformation polymorphism.

23.-24. (Canceled)